

[illegible]

FIG. 1

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Interleukin-22

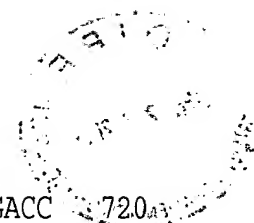
1 GGAATTCGGCACGAGCTCGTGCCGTGCTCAGTGCCTTCCACCACACGCTGCAGCTGGGGC 60
1 N S A R A R A V L S A F H H T L Q L G P 20

61 CGCGTGAGCAGGCGCGCAACGCGAGCTGCCCCGCGAGGGGGCAGGCCCCGCGACCGCCGCT 120
21 R E Q A R N A S C P A G G R P A D R R F 40
121 TCCGGCCGCCACCAACCTGCGCAGCGTGTGCCCCTGGGCCTACAGAATCTCCTACGACC 180
41 R P P T N L R S V S P W A Y R I S Y D P 60
Domain I
181 CGGCGAGGTACCCAGGTACCTGCCTGAAGCCTACTGCCTGTGCCGGGGCTGCCTGACCG 240
61 A R Y P R Y L P E A Y C L C R G C L T G 80
Domain I Domain II
241 GGCTGTTCCGGCAGGAGGACGTGCGCTTCCGAGCGCCCCTGTCTACATGCCACCGTCCG 300
81 L F G E E D V R F R S A P V Y M P T V V 100
Domain III
301 TCCTGCGCCGCACCCCGCCTGCGCCGGCGGCCGTTCCGTCTACACCGAGGCCTACGTCA 360
101 L R R T P A C A G G R S V Y T E A Y V T 120
Domain III

361 CCATCCCCGTGGGCTGCACCTGCGTCCCCGAGCCGGAGAAGGACGCAGACAGCATCAACT 420
121 I P V G C T C V P E P E K D A D S I N S 140
Domain IV
421 CCAGCATCGACAAACAGGGCGCCAAGCTCCTGCTGGGCCCCAACGACGCGCCCGCTGGCC 480
141 S I D K Q G A K L L L G P N D A P A G P 160
481 CCTGAGGCCGGTCCCTGCCCCGGGAGGTCTCCCCGGCCCGCATCCCAGGGCGCCAAGCTG 540
541 GAGCCGCCTGGAGGGCTCGGTGCGCGACCTCTGAAGAGAGTGCACCGAGCAAACCAAGTG 600
601 CCGGAGCACCAGCGCCGCTTTCCATGGAGACTCGTAAGCAGCTTCATCTGACACGGGCA 660

FIG. 2A

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Interleukin-22



661 TCCCTGGCTTGCTTTTAGCTACAAGCAAGCAGCGTGGCTGGAAGCTGATGGGAAACGACC 720
721 CGGCACGGGCATCCTGTGTGCGGCCCGCATGGAGGGTTTGAAAAGTTCACGGAGGCTCC 780
781 CTGAGGAGCCTCTCAGATCGGCTGCTGCGGGTGCAAGGCGTGACTIONACCGCTGGGTGCTT 840
841 GCCAAAGAGATAGGGACGCATATGCTTTTTAAAGCAATCTAAAAATAATAAAGTATAG 900
901 CGACTATATACCTACTTTTAAATCAACTGTTTTGAATAGAGGCAGAGCTATTTTATATT 960
961 ATCAAATGAGAGCTACTCTGTTACATTTCTTAACATATAAACATCGTTTTTTACTTCTTC 1020
1021 TGGTAGAATTTTTTAAAGCATAATTGGAATCCTTGGATAAATTTTGTAGCTGGTACACTC 1080
1081 TGGCCTGGGTCTCTGAATTCAGCCTGTCACCGATGGCTGACTGATGAAATGGACACGTCT 1140
1141 CATCTGACCCACTCTTCCTTCCACTGAAGGTCTTCACGGGCCTCCAGGTGGACCAAAGGG 1200
1201 ATGCACAGGCGGCTCGCATGCCCCAGGGCCAGCTAAGAGTTCCAAAGATCTCAGATTTGG 1260
1261 TTTTAGTCATGAATACATAAACAGTCTCAAACCTCGCACAATTTTTTCCCCCTTTTGAAAG 1320
1321 CCACTGGGGCCAATTTGTGGTTAAGAGGTGGTGAGATAAGAAGTGAACGTGACATCTTT 1380
1381 GCCAGTTGTGAGAAGAATCCAAGCAGGTATTGGCTTAGTTGTAAGGGCTTTAGGATCAGG 1440
1441 CTGAATATGAGGACAAAGTGGGCCACGTTAGCATCTGCAGAGATCAATCTGGAGGCTTCT 1500
1501 GTTTCTGCATTCTGCCACGAGAGCTAGGTCCTTGATCTTTTCTTTAGATTGAAAGTCTGT 1560
1561 CTCTGAACACAATTATTTGTAAAAGTTAGTAGTTCTTTTTTAAATCATTAAAAGAGGCTT 1620
1621 GCTGAAAAAAAAAAAAAAAAAAAA 1642

FIG. 2B

	60	70	80	90	100
39	- - - - -	KNFPR	TVMLNI - HNRN	TNTNP	KRSSDY - - - - - II-17.aa
41	- - - - -	KDFLQ	NVKVFN	SLGAKVSS	RRPSPDY - - - - - mII-17.aa
38	- - - - -	SFPR	SVMTLSI - RNWN	TSS - SKR	ASDY - - - - - vII-17.aa
51	SRMKPYARMEEYERNIE - EMVAQ	LNRNSSELAQR	- - - - -	KCEV	- - - - - N II20.aa
2	- - - - -	- - - - -	- - - - -	- - - - -	- - - - - II-21.aa
48	PP - HLLARGAKWGQALP	VALVSSLEAASHRG	HERPSATQ	CPVL - RPEE	II21FL.aa
5	- - - - -	ARAVLSAFHHTLQ	LGPREQARNAS	- CPAGGRPAD	II-22.aa
12	- - - - -	LAAGVLSAFHHTLQ	LGPREQARNAS	- CPAGGRPAD	II22ext.aa

	160	170	180	190	200
109	H M N S V P I Q Q E I L V L R R E P	- - - - - P H C P N S F R L E K I L	- - - - - V S V G C T C V	T P	II-17.aa
112	H M N S V L I Q Q E I L V L K R E P	- - - - - E S C P F T F R V E K M L	- - - - - V G V G C T C V	A S	mII-17.aa
105	H M N S V P I Q Q E I L V V R K G H	- - - - - Q P C P N S F R L E K M L	- - - - - V T V G C T C V	T P	vII-17.aa
137	S M V S V P V F - S Q V P V R R R L C	P P P P R T G P C R Q - - - - R A V M E T	I A V G C T C I	- -	II20.aa
35	A L N S V R L L Q S L L V L R R R P C	S R D G S G L P T P G A F A F H T E F I H	V P V G C T C V	- -	II-21.aa
145	A L N S V R L L Q S L L V L R R R P C	S R D G S G L P T P G A F A F H T E F I H	V P V G C T C V	- -	II21FL.aa
88	R F R S A P V Y M P T V V L R R T	P A C A G R S V - - - - - Y T E A Y V T	I P V G C T C V	P E	II-22.aa
101	R F R S A P V Y M P T V V L R R T	P A C A G R S V - - - - - Y T E A Y V T	I P V G C T C V	P E	II22ext.aa

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IL-17.aa
 mIL-17.aa
 vIL-17.aa
 IL20.aa
 IL-21.aa
 IL21FL.aa
 IL-22.aa
 IL22ext.aa

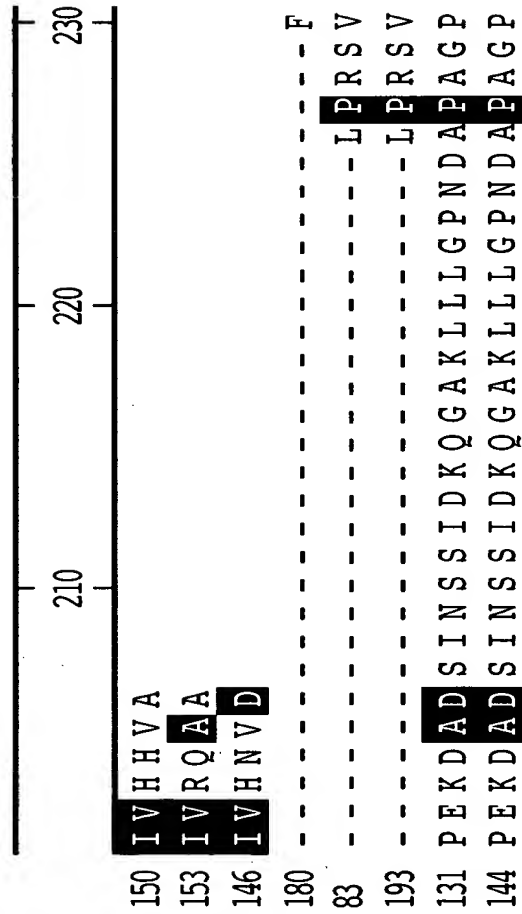


FIG. 3C

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Interleukin-21 Polypeptide Analysis

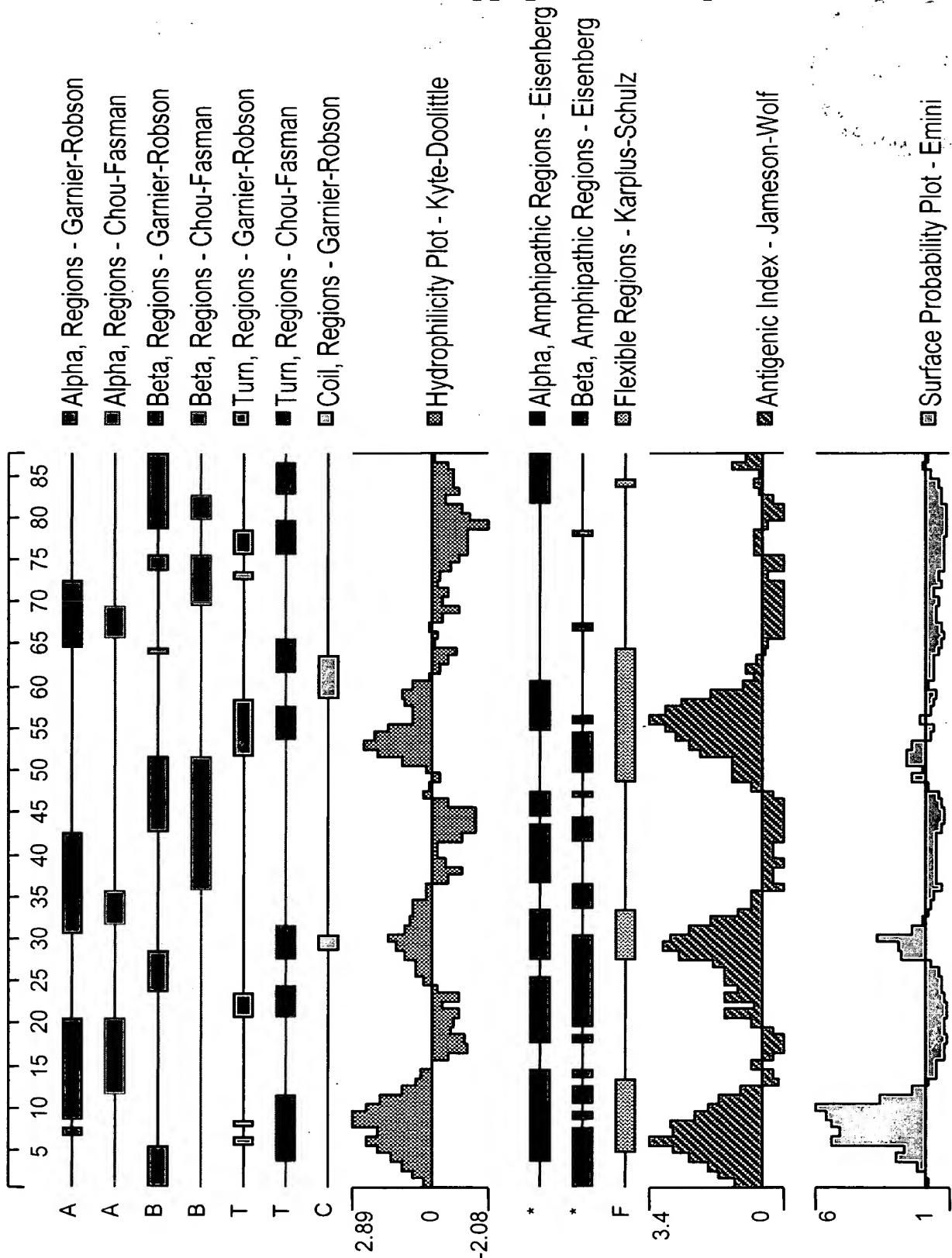


FIG. 4

Interleukin-22 Polypeptide Analysis

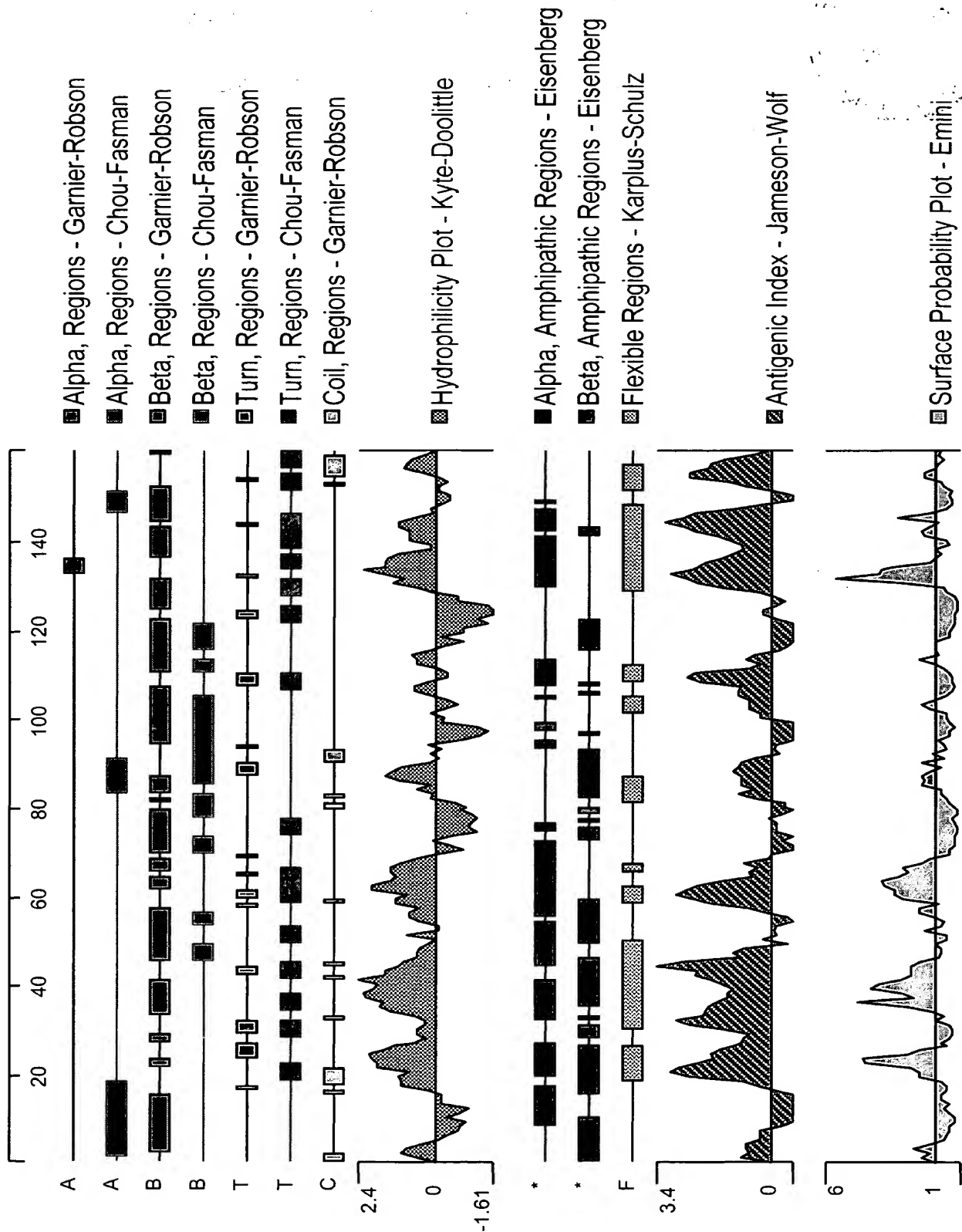


FIG. 5

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Interleukin-21

1 GCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCCCCGGCCTCCTGTTT 60
 1 M T L L P G L L F 9

61 CTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGGGCACCCCCAC 120
 10 L T W L H T C L A H H D P S L R G H P H 29

121 AGTCACGGTACCCACACTGCTACTCGGCTGAGGAACTGCCCTCGGCCAGGCCCCCCCCA 180
 30 S H G T P H C Y S A E E L P L G Q A P P 49
Domain V

181 CACCTGCTGGCTCGAGGTGCCAAGTGGGGGAGGCTTTGCCTGTAGCCCTGGTGTCCAGC 240
 50 H L L A R G A K W G Q A L P V A L V S S 69
Domain VI

241 CTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGCCCCG 300
 70 L E A A S H R G R H E R P S A T T Q C P 89

301 GTGCTGCGGCCGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACCCCTGG 360
 90 V L R P E E V L E A D T H Q R S I S P W 109
Domain VII

361 AGATACCGGGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGC 420
 110 R Y R V D T D E D R Y P Q K L A F A E C 129
Domain I *Domain II*

421 CTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTG 480
 130 L C R G C I D A R T G R E T A A L N S V 149
Domain II

481 CGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGG 540
 150 R L L Q S L L V L R R R P C S R D G S G 169
Domain III

541 CTCCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTGCGCTGC 600
 170 L P T P G A F A F H T E F I H V P V G C 189
Domain IV

FIG. 6A

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Interleukin-21

601 ACCTGCGTGCTGCCCCGTTTCAGTGTGACCGCCAAGGCCGTGGGGCCCTTAGACTGGACAC 660
190 T C V L P R S V 197
Domain IV
661 GTGTGCTCCCCAGAGGGCACCCCCTATTTATGTGTATTTATTGTTATTTATATGCCTCCC 720
721 CCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGACAGCCCCCACTGTTC 780
781 TCCTCATCTCCAGCCTCAGTAGTTGGGGGTWGAAGGAGCTCAGCACCTCTCCAGCCCTT 840
841 AAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGYTCCCTGTCCTGCTCCCGG 900
901 CTTCCCTTACCCTATCACTGGCCTCAGGCCCCCGCAGGCTGCCTCTTCCCAACCTCCTTG 960
961 GAAGTACCCCTGTTTCTTAAACAATTATTTAAGTGTACGTGTATTATTAAACTGATGAAC 1020
1021 ACAA 1067

FIG. 6B

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Interleukin-21 Polypeptide Analysis

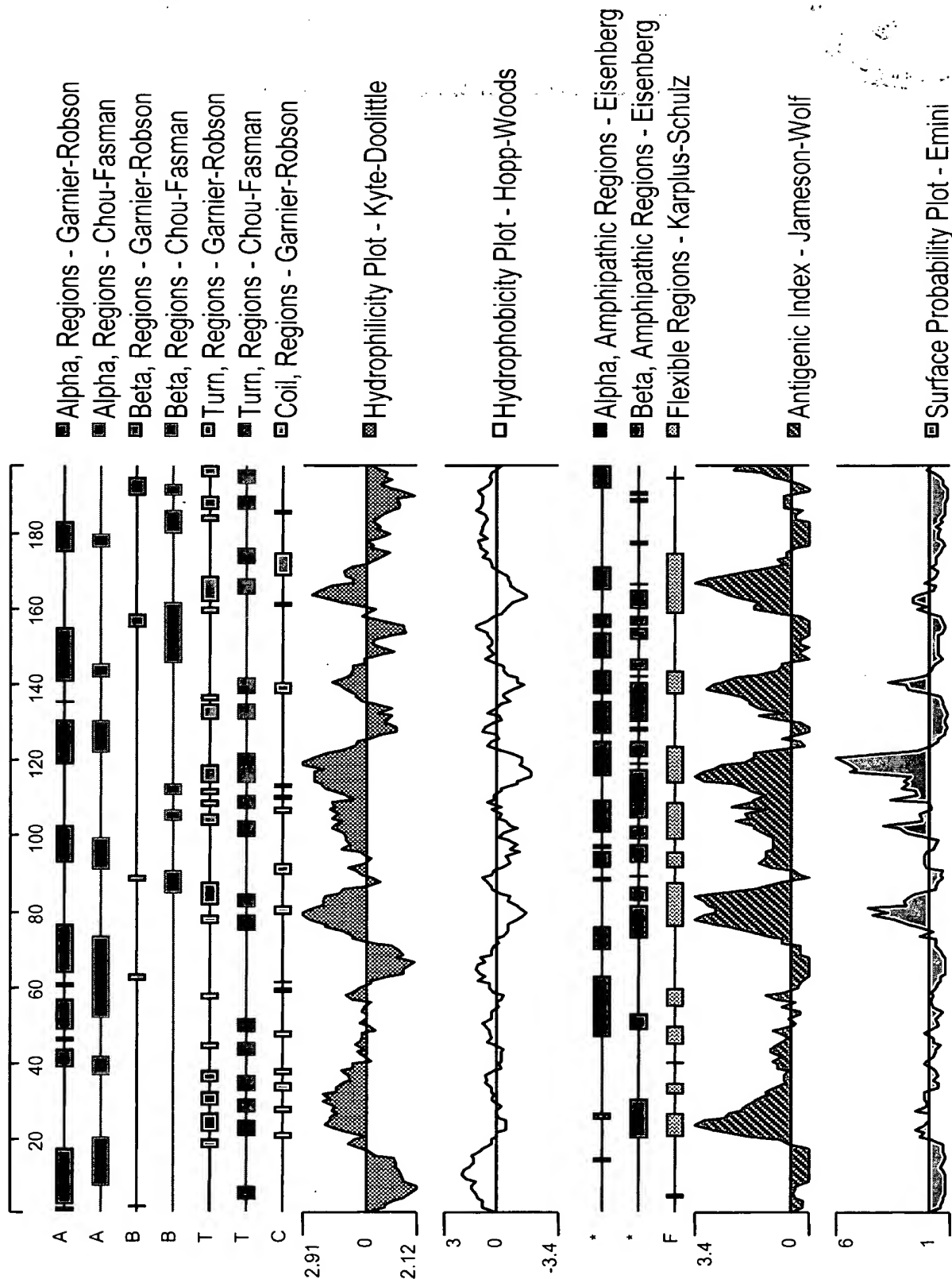


FIG. 7

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Interleukin-22

1 GGCTGCGCGGACCGGCCGGAGGAGCTACTGGAGCAGCTGTACGGGCGCCTGGCGGCCGGC 60
 1 G C A D R P E E L L E Q L Y G R L A A G 20
 CD-VI
 #
 61 GTGCTCAGTGCCTTCCACCACACGCTGCAGCTGGGGCCGCGTGAGCAGGCGCGCAACGCG 120
 21 V L S A F H H T L Q L G P R E Q A R N A 40
 CD-VI
 121 AGCTGCCCCGAGGGGGCAGGCCCCGCCACCGCCGCTTCCGGCCGCCACCAACCTGCGC 180
 41 S C P A G G R P A D R R F R P P T N L R 60
 181 AGCGTGTGCCCCTGGGCCTACAGAATCTCCTACGACCCGGCGAGGTACCCCAGGTACCTG 240
 61 S V S P W A Y R I S Y D P A R Y P R Y L 80
 CD-VII CD-I
 241 CCTGAAGCCTACTGCCTGTGCCGGGGCTGCCTGACCGGGCTGTTCCGGCGAGGAGGACGTG 300
 81 P E A Y C L C R G C L T G L F G E E D V 100
 CD-II
 301 CGCTTCCGCAGCGCCCCTGTCTACATGCCCACCGTCGTCTGCGCCGCACCCCCGCCTGC 360
 101 R F R S A P V Y M P T V V L R R T P A C 120
 CD-III
 361 GCCGGCGGCCGTTCCGTCTACACCGAGGCCTACGTCACCATCCCCGTGGGCTGCACCTGC 420
 121 A G G R S V Y T E A Y V T I P V G C T C 140
 CD-IV
 #
 421 GTCCCCGAGCCGAGAAGGACGCAGACAGCATCAACTCCAGCATCGACAAACAGGGCGCC 480
 141 V P E P E K D A D S I N S S I D K Q G A 160
 CD-IV
 481 AAGCTCCTGCTGGGCCCCAACGACGCGCCCGCTGGCCCTGA 522
 161 K L L L G P N D A P A G P 174

FIG. 8

Interleukin-22 Polypeptide Analysis

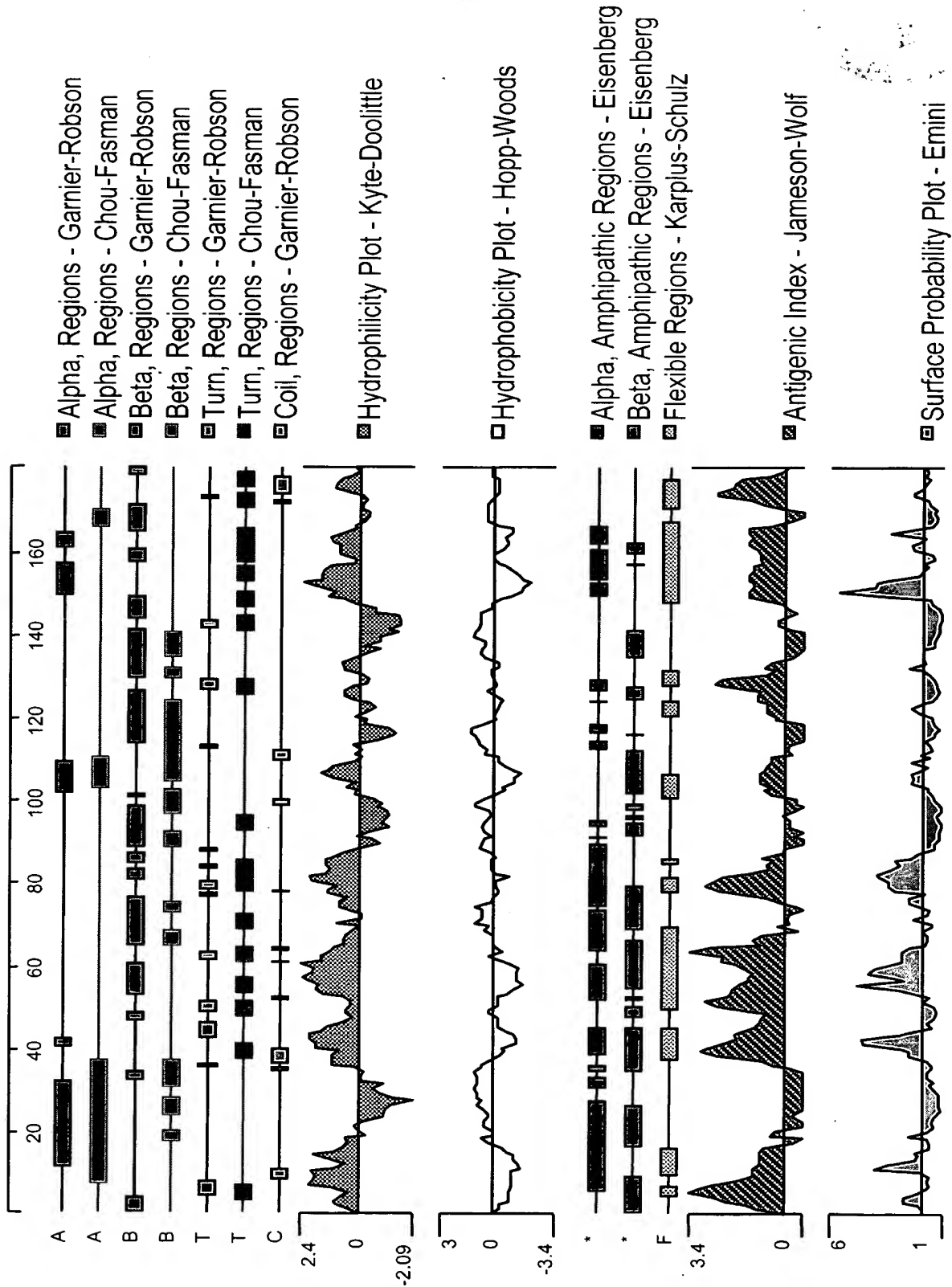


FIG. 9